

**Amendments to the Claims/Listing of Claims**

Please amend claims 14, 15, 18, 19, 20, 31 and 32, and add new claims 38-39 as follows. In addition, please cancel claims 1-3, 6-13, 21, 22 and 33 without prejudice. This listing of claims will replace all prior versions, and listings, of claims in the application:

1. - 13. Cancelled

14. (Currently amended) A method of screening molecules to determine those which are capable of binding to a farnesoid X receptor (FXR) molecule, said method comprising: modeling a test molecule that potentially interacts with [[a]] the ligand binding domain of [[a]] said farnesoid X receptor (FXR) molecule, said ligand binding domain comprising amino acid residues 248 - 476 of SEQ ID NO:1,

wherein said ligand binding domain is further defined by ~~a plurality of the structure coordinates of the ligand binding domain of a FXR molecule or a fragment thereof, and~~

~~wherein said structure coordinates are based on X-ray diffraction data obtained from crystals of said FXR molecule or molecular complex, or a homologue of said FXR molecule or molecular complex, set forth in Appendix 1, or a portion thereof sufficient to define the points of interaction between said ligand binding domain and a ligand therefor, and~~

determining whether there is repulsive electrostatic interaction between said test molecule and said FXR molecule,

whereby those ~~compounds~~ test molecules which lack repulsive electrostatic interaction with said FXR molecule in their bound state are capable of binding to a farnesoid X receptor (FXR) molecule ~~therefor~~.

15. (Currently amended) A method according to claim 14, wherein said ~~plurality of~~ structure coordinates are ~~as~~ set forth in Appendix 1, ~~or a portion thereof sufficient to define the points of interaction between said ligand binding domain and a ligand therefor.~~

16.-17. Cancelled.

18. (Currently amended) A method according to claim 14, wherein said test molecule is developed using a computer algorithm to predict a three-dimensional representation of said test molecule interacting with a FXR molecule based upon a three-dimensional representation of a FXR molecule ~~or fragment thereof.~~

19. (Currently amended) A method of screening compounds to determine those with agonist, partial agonist, or antagonist activity with respect to a farnesoid X receptor (FXR) molecule, said method comprising:

(a) modeling a test compound that potentially interacts with [[a]] the ligand binding domain of [[a]] said farnesoid X receptor (FXR) molecule, said ligand binding domain comprising amino acid residues 248 - 476 of SEQ ID NO:1,

wherein said ligand binding domain is further defined by ~~a plurality of the~~ structure coordinates ~~of a crystalline form of the ligand binding domain of a FXR molecule or a fragment thereof, and~~

~~wherein said plurality of structure coordinates are based on X-ray diffraction data obtained from crystals of said FXR molecule or molecular complex, or a homologue of said FXR molecule or molecular complex set forth in Appendix 1, or a portion thereof sufficient to define the points of interaction between said ligand binding domain and a ligand therefor;~~

and

(b) determining the ability of said test compound to modulate the activity of said FXR molecule in the optional presence of a known FXR agonist,

whereby those **molecules test compounds** which bind and alter the activity of farnesoid X receptor (FXR) molecule are identified as agonists or partial agonists, and those **test** compounds which bind but do not alter the activity of farnesoid X receptor (FXR) molecule are identified as antagonists therefor.

20. (Currently amended) A method according to claim 19, wherein said **plurality of** structure coordinates are as set forth in Appendix 1, or a portion thereof sufficient to define the points of interaction between said ligand binding domain and a ligand therefor.

21. - 30. Cancelled

31. (Withdrawn; currently amended) A method for determining whether a test compound is capable of binding to the ligand binding domain of a farnesoid X receptor (FXR) molecule comprising amino acid residues 248 – 476 of SEQ ID NO:1, said method comprising:

(a) determining the points of interaction between a crystalline form of the ligand binding domain of a FXR, and one or more known ligand(s) therefore utilizing structure coordinates derived from X-ray diffraction data obtained from crystals of said FXR molecule or molecular complex thereof to define said points of interaction, wherein said structure coordinates are set forth in Appendix 1, or a portion thereof sufficient to define the points of interaction between said ligand binding domain and said ligand(s); and

(b) analyzing said test compound to determine whether similar points of interaction exist between said test compound and said ligand binding domain.

32. (Withdrawn; currently amended) A method according to claim 31, wherein step (a) utilizes a plurality of for determining whether a test compound is capable of binding to the ligand binding domain of a farnesoid X receptor (FXR) molecule comprising amino acid residues 248 – 476 of SEQ ID NO:1, said method comprising:

(a) determining the points of interaction between a crystalline form of the ligand binding domain of a FXR molecule and one or more known ligand(s) therefore utilizing structure coordinates derived from X-ray diffraction data obtained from crystals of said FXR molecule or molecular complex ~~or a homologue of said FXR molecule or molecular complex thereof~~ to define said points of interaction, wherein the crystals belong to space group P2<sub>1</sub>2<sub>1</sub>2<sub>1</sub> with unit cell dimensions of about:

$$a = 37 \text{ \AA}, b = 57 \text{ \AA}, c = 117 \text{ \AA}, \\ \alpha = 90^\circ, \beta = 90^\circ, \text{ and } \gamma = 90^\circ, \text{ and}$$

(b) analyzing said test compound to determine whether similar points of interaction exist between said test compound and said ligand binding domain.

33.-37. Cancelled.

38. (New) A method of screening molecules to determine those which are capable of binding to a farnesoid X receptor (FXR) molecule, said method comprising:

modeling a test molecule that potentially interacts with the ligand binding domain of said farnesoid X receptor (FXR) molecule, said ligand binding domain comprising amino acid residues 248 - 476 of SEQ ID NO:1,

wherein said ligand binding domain is further defined by the structure coordinates of the ligand binding domain of a FXR molecule,

wherein said structure coordinates are based on X-ray diffraction data obtained from crystals of said FXR molecule or molecular complex thereof, and

wherein the crystals belong to space group P2<sub>1</sub>2<sub>1</sub>2<sub>1</sub> with unit cell dimensions of about:

$$a = 37 \text{ \AA}, b = 57 \text{ \AA}, c = 117 \text{ \AA}, \\ \alpha = 90^\circ, \beta = 90^\circ, \text{ and } \gamma = 90^\circ, \text{ and}$$

determining whether there is repulsive electrostatic interaction between said test molecule and said FXR molecule,

whereby those compounds which lack repulsive electrostatic interaction with FXR molecule in their bound state are capable of binding to a farnesoid X receptor (FXR) molecule therefor.

39. (New) A method of screening compounds to determine those with agonist, partial agonist, or antagonist activity with respect to a farnesoid X receptor (FXR) molecule, said method comprising:

(a) modeling a test compound that potentially interacts with the ligand binding domain of said FXR molecule, said ligand binding domain comprising amino acid residues 248 - 476 of SEQ ID NO:1,

wherein said ligand binding domain is defined by the structure coordinates of a crystalline form of the ligand binding domain of a FXR molecule,

wherein said structure coordinates are based on X-ray diffraction data obtained from crystals of said FXR molecule or molecular complex, and

wherein the crystals belong to space group  $P2_12_12_1$  with unit cell dimensions of about:

$$a = 37 \text{ \AA}, b = 57 \text{ \AA}, c = 117 \text{ \AA},$$

$$\alpha = 90^\circ, \beta = 90^\circ, \text{ and } \gamma = 90^\circ; \text{ and}$$

(b) determining the ability of said test compound to modulate the activity of said FXR molecule in the optional presence of a known FXR agonist,

whereby those test compounds which bind and alter the activity of farnesoid X receptor (FXR) molecule are identified as agonists or partial agonists, and those test compounds which bind but do not alter the activity of farnesoid X receptor (FXR) molecule are identified as antagonists therefor.